Exhibit A

Databases   Tools

All Databases | Enter Text Here | Reset ② | Advanced Search

Groups   Training   Industry   About Us   Help

Help
General Help
Formats
Gaps
Matrix
References
EMBOSS-Align Help

EMBOSS Align Results

Needle Results

Matrix	Blosum62
Open gap penalty	10.0
Gap extension penalty	0.5
Needle output	needle-20070226-19371266036393.output

SUBMIT ANOTHER JOB

```
########################################
# Program:  needle
# Rundate:  Mon Feb 26 19:37:13 2007
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20070226-19371266036393.output
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 524
# Identity:     414/524 (79.0%)
# Similarity:   451/524 (86.1%)
# Gaps:          23/524 ( 4.4%)
# Score: 2064.0
#
#
#=======================================
```

018512- 00/420 ns (handwritten)

Mouse SEQ 1 (handwritten)
human SEQ 17 (handwritten)

```
EMBOSS_001         1 MPMSSRDRDLHPGHHHFGSCSPLSQLWPGP-EPKSVKGLYYSRARKVGNQ     49
                     |||.|||..|||.|||:||-||.|||...| |..:|||||.|.||||..
EMBOSS_001         1 MPMPSRDGGLHPRHHYGSHSPWSQLLSSPMETPSIKGLYYRRVRKVGAL     50

EMBOSS_001        50 DASPEANLKEILVNVGGQRYLLPWSTLDAFPLSRLSRLRLCRSHEEITQL     99
                     ||||....||||:|||||:|||||||||||.||||||:||||||:|||.||
EMBOSS_001        51 DASPVDLKKEILINVGGRRYLLPWSTLDRFPLSRLSKLRLCRSYEEIVQL    100

EMBOSS_001       100 CDDYDEDSQEFFFDRNPSAFGVIVSFLAAGKLVLLREMCALSFREELSYW    149
                     |||||||||||||||:||||||||||||||||||||:|||||||:|||:||
EMBOSS_001       101 CDDYDEDSQEFFFDRSPSAFGVIVSFLAAGKLVLLQEMCALSFQEELAYW    150

EMBOSS_001       150 GIEETNLERCCLRKLLKK---LEEAAELRREEA--AQRQQQRQACHSEVQ    194
                     ||||..:|||||||||||:| |||.|:|.||:. .||::.:|.|.||
EMBOSS_001       151 GIEEAHLERCCLRKLLRKLEELEELAKLHREDVLRQQQRETRRPASHS---    197

EMBOSS_001       195 ASRWARSMNQLREMVEDPQSGLPGKVFACLSVLFVATTAVSLCVSTMPDF    244
                     |||...||:|||||||:||||||||||||||:||||||||||||||||||.
EMBOSS_001       198 -SRWGLCMNRLREMVENPQSGLPGKVFACLSILFVATTAVSLCVSTMPDL    246

EMBOSS_001       245 RAEEGKGECTRKCYYIFVVESICVAWFSLEFCLRFVQAPNKCQFFRGPLN    294
                     ||||.:||||:|||||||:||:||||||||||||||||..:||||:||||
EMBOSS_001       247 RAEEDQGECSRKCYYIFIVETICVAWFSLEFCLRFVQAQDKCQFFQGPLN    296

EMBOSS_001       295 VIDILAISPYYVSLAVSDESPEAGERPSSSSYLEKVGLVLRVLRALRILY    344
```

```
                         :|||||||||||||||||:|·||·|||||·||||||||||||||||||||
EMBOSS_001       297 IIDILAISPYYVSLAVSEEPPEDGERPSRSSYLEKVGLVLRVLRALRILY       346


EMBOSS_001       345 VMRLARHSLGLQTLGLTVRRCAREFGLLMLFLAVAVTLFSPLVYVAENES       394
                         ||||||||||||||||||||||··|||||:|||||||:|||||||||||·||
EMBOSS_001       347 VMRLARHSLGLQTLGLTVRRCTCEFGLLLLFLAVAITLFSPLVYVAEKES       396

EMBOSS_001       395 GRVLEFTSIPASYWWAIISMTTVGYGDMVPRSVPGQMVALSSILSGILIM       444
                         ||||||||||||||||||||||||||||||||||||||||||||||||||
EMBOSS_001       397 GRVLEFTSIPASYWWAIISMTTVGYGDMVPRSVPGQMVALSSILSGILIM       446

EMBOSS_001       445 AFPATSIFHTFSHSY-ELKVREQEQVQARLRRLQNT-----------NSA       482
                         |||||||||||||| |||  :||||:|||||·||||               :·|
EMBOSS_001       447 AFPATSIFHTFSHSYLELK-KEQEQLQARLRHLQNTGPASECELLDPHVA       495

EMBOSS_001       483 SERELLSDVDDLVPEGLTSPGRYM      506
                         ||·||::||:||:·||···|··:|
EMBOSS_001       496 SEHELMNDVNDLILEGPALPIMHM      519
```

```
#---------------------------------------
#---------------------------------------
```